

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/539,723
Source: PG/10
Date Processed by STIC: 7/12/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 07/12/2005

PATENT APPLICATION: US/10/539,723

TIME: 10:02:55

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Output Set: N:\CRF4\07122005\J539723.raw

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3 <110> APPLICANT: Bayer CropScience GmbH
5 <120> TITLE OF INVENTION: Plant cells and plants which synthesize a starch with an
increased final
6     viscosity
8 <130> FILE REFERENCE: BCS 02 5002 - PCT
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/539,723
C--> 10 <141> CURRENT FILING DATE: 2005-06-20
10 <150> PRIOR APPLICATION NUMBER: EP 02028530.0
11 <151> PRIOR FILING DATE: 2002-12-19
13 <150> PRIOR APPLICATION NUMBER: EP 03090275.3
14 <151> PRIOR FILING DATE: 2003-08-29
16 <160> NUMBER OF SEQ ID NOS: 8
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 4167
22 <212> TYPE: DNA
23 <213> ORGANISM: Solanum tuberosum
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (207)..(3899)
28 <223> OTHER INFORMATION:
31 <300> PUBLICATION INFORMATION:
32 <301> AUTHORS: Abel,G.J., Springer,F., Willmitzer,L. and Kossmann,J.
33 <302> TITLE: Cloning and functional analysis of a cDNA encoding a novel 139 kDa
34 <303> JOURNAL: Plant J.
35 <304> VOLUME: 10
36 <305> ISSUE: 6
37 <306> PAGES: 981-991
38 <307> DATE: 1996
39 <308> DATABASE ACCESSION NO: X94400
40 <309> DATABASE ENTRY DATE: 1995-12-22
41 <313> RELEVANT RESIDUES: (1)..(4167)
43 <300> PUBLICATION INFORMATION:
44 <308> DATABASE ACCESSION NO: EMBL / X94400
45 <309> DATABASE ENTRY DATE: 1997-04-16
46 <313> RELEVANT RESIDUES: (1)..(4167)
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53 gatgttctat ttgattctgt ggtgaacaag agttttacaa agaacattcc tttttctttt      180
55 tttcttggtt cttgtgtggg tcagcc atg gat gtt cca ttt cca ctg cat aga      233
56                                     Met Asp Val Pro Phe Pro Leu His Arg
57                                     1                               5
59 cca ttg agt tgc aca agt gtc tcc aat gca ata acc cac ctc aag atc      281

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61 10          15          20          25
63 aaa cct ttt ctt ggg ttt gtc tct cat gga acc aca agt cta tca gta      329
64 Lys Pro Phe Leu Gly Phe Val Ser His Gly Thr Thr Ser Leu Ser Val
65          30          35          40
67 caa tct tct tca tgg agg aag gat gga atg gtt act ggg gtt tca ttt      377
68 Gln Ser Ser Ser Trp Arg Lys Asp Gly Met Val Thr Gly Val Ser Phe
69          45          50          55
71 cca ttt tgt gca aat ctc tcg gga aga aga cgg aga aaa gtt tca act      425
72 Pro Phe Cys Ala Asn Leu Ser Gly Arg Arg Arg Arg Lys Val Ser Thr
73          60          65          70
75 act agg agt caa gga tct tca cct aag ggg ttt gtg cca agg aag ccc      473
76 Thr Arg Ser Gln Gly Ser Ser Pro Lys Gly Phe Val Pro Arg Lys Pro
77          75          80          85
79 tca ggg atg agc acg caa aga aag gtt cag aag agc aat ggt gat aaa      521
80 Ser Gly Met Ser Thr Gln Arg Lys Val Gln Lys Ser Asn Gly Asp Lys
81 90          95          100          105
83 gaa agt caa agt act tca aca tct aaa gaa tct gaa att tcc aac cag      569
84 Glu Ser Gln Ser Thr Ser Thr Ser Lys Glu Ser Glu Ile Ser Asn Gln
85          110          115          120
87 aag acg gtt gaa gca aga gtt gaa act agt gac gat gac act aaa gta      617
88 Lys Thr Val Glu Ala Arg Val Glu Thr Ser Asp Asp Asp Thr Lys Val
89          125          130          135
91 gtg gtg agg gac cac aag ttt ctg gag gat gag gat gaa atc aat ggt      665
92 Val Val Arg Asp His Lys Phe Leu Glu Asp Glu Asp Glu Ile Asn Gly
93          140          145          150
95 tct act aaa tca ata agt atg tca cct gtt cgt gta tca tct caa ttt      713
96 Ser Thr Lys Ser Ile Ser Met Ser Pro Val Arg Val Ser Ser Gln Phe
97          155          160          165
99 gtt gaa agt gaa gaa act ggt ggt gat gac aag gat gct gta aag tta      761
100 Val Glu Ser Glu Glu Thr Gly Gly Asp Asp Lys Asp Ala Val Lys Leu
101 170          175          180          185
103 aac aaa tca aag aga tcg gaa gag agt gat ttt cta att gat tct gta      809
104 Asn Lys Ser Lys Arg Ser Glu Glu Ser Asp Phe Leu Ile Asp Ser Val
105          190          195          200
107 ata aga gaa caa agt gga tct cag ggg gaa act aat gcc agt agc aag      857
108 Ile Arg Glu Gln Ser Gly Ser Gln Gly Glu Thr Asn Ala Ser Ser Lys
109          205          210          215
111 gga agc cat gct gtg ggt aca aaa ctt tat gag ata ttg cag gtg gat      905
112 Gly Ser His Ala Val Gly Thr Lys Leu Tyr Glu Ile Leu Gln Val Asp
113          220          225          230
115 gtt gag cca caa caa ttg aaa gaa aat aat gct ggg aat gtt gaa tac      953
116 Val Glu Pro Gln Gln Leu Lys Glu Asn Asn Ala Gly Asn Val Glu Tyr
117          235          240          245
119 aaa gga cct gta gca agt aag cta ttg gaa att act aag gct agt gat      1001
120 Lys Gly Pro Val Ala Ser Lys Leu Leu Glu Ile Thr Lys Ala Ser Asp
121 250          255          260          265
123 gtg gaa cac act gaa agc aat gag att gat gac tta gac act aat agt      1049
124 Val Glu His Thr Glu Ser Asn Glu Ile Asp Asp Leu Asp Thr Asn Ser

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128	Phe Phe Lys Ser Asp Leu Ile Glu Glu Asp Glu Pro Leu Ala Ala Gly						
129		285		290		295	
131	aca gtg gag act gga gat tct tct cta aac tta aga ttg gag atg gaa						1145
132	Thr Val Glu Thr Gly Asp Ser Ser Leu Asn Leu Arg Leu Glu Met Glu						
133		300		305		310	
135	gca aat cta cgt agg cag gct ata gaa agg ctt gcc gag gaa aat tta						1193
136	Ala Asn Leu Arg Arg Gln Ala Ile Glu Arg Leu Ala Glu Glu Asn Leu						
137		315		320		325	
139	ttg caa ggg atc aga tta ttt tgt ttt cca gag gtt gta aaa cct gat						1241
140	Leu Gln Gly Ile Arg Leu Phe Cys Phe Pro Glu Val Val Lys Pro Asp						
141	330		335		340	345	
143	gaa gat gtc gag ata ttt ctt aac aga ggt ctt tcc act ttg aag aat						1289
144	Glu Asp Val Glu Ile Phe Leu Asn Arg Gly Leu Ser Thr Leu Lys Asn						
145		350		355		360	
147	gag tct gat gtc ttg att atg gga gct ttt aat gag tgg cgc tat agg						1337
148	Glu Ser Asp Val Leu Ile Met Gly Ala Phe Asn Glu Trp Arg Tyr Arg						
149		365		370		375	
151	tct ttt act aca agg cta act gag act cat ctc aat gga gat tgg tgg						1385
152	Ser Phe Thr Thr Arg Leu Thr Glu Thr His Leu Asn Gly Asp Trp Trp						
153		380		385		390	
155	tct tgc aag atc cat gtt ccc aag gaa gca tac agg gct gat ttt gtg						1433
156	Ser Cys Lys Ile His Val Pro Lys Glu Ala Tyr Arg Ala Asp Phe Val						
157		395		400		405	
159	ttt ttt aat gga caa gat gtc tat gac aac aat gat gga aat gac ttc						1481
160	Phe Phe Asn Gly Gln Asp Val Tyr Asp Asn Asn Asp Gly Asn Asp Phe						
161	410		415		420	425	
163	agt ata act gtg aaa ggt ggt atg caa atc att gac ttt gaa aat ttc						1529
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167	ttg ctt gag gag aaa tgg aga gaa cag gag aaa ctt gct aaa gaa caa						1577
168	Leu Leu Glu Glu Lys Trp Arg Glu Gln Glu Lys Leu Ala Lys Glu Gln						
169		445		450		455	
171	gct gaa aga gaa aga cta gcg gaa gaa caa aga cga ata gaa gca gag						1625
172	Ala Glu Arg Glu Arg Leu Ala Glu Glu Gln Arg Arg Ile Glu Ala Glu						
173		460		465		470	
175	aaa gct gaa att gaa gct gac aga gca caa gca aag gaa gag gct gca						1673
176	Lys Ala Glu Ile Glu Ala Asp Arg Ala Gln Ala Lys Glu Glu Ala Ala						
177		475		480		485	
179	aag aaa aag aaa gta ttg cga gaa ttg atg gta aaa gcc acg aag act						1721
180	Lys Lys Lys Lys Val Leu Arg Glu Leu Met Val Lys Ala Thr Lys Thr						
181	490		495		500	505	
183	cgt gat atc acg tgg tac ata gag cca agt gaa ttt aaa tgc gag gac						1769
184	Arg Asp Ile Thr Trp Tyr Ile Glu Pro Ser Glu Phe Lys Cys Glu Asp						
185		510		515		520	
187	aag gtc agg tta tac tat aac aaa agt tca ggt cct ctc tcc cat gct						1817
188	Lys Val Arg Leu Tyr Tyr Asn Lys Ser Ser Gly Pro Leu Ser His Ala						
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191	aag	gac	ttg	tgg	atc	cac	gga	gga	tat	aat	aat	tgg	aag	gat	ggt	ttg	1865
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196	Ser	Ile	Val	Lys	Lys	Leu	Val	Lys	Ser	Glu	Arg	Ile	Asp	Gly	Asp	Trp	
197		555					560						565				
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200	Trp	Tyr	Thr	Glu	Val	Val	Ile	Pro	Asp	Gln	Ala	Leu	Phe	Leu	Asp	Trp	
201	570					575					580					585	
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204	Val	Phe	Ala	Asp	Gly	Pro	Pro	Lys	His	Ala	Ile	Ala	Tyr	Asp	Asn	Asn	
205				590						595					600		
207	cac	cgc	caa	gac	ttc	cat	gcc	att	gtc	ccc	aac	cac	att	ccg	gag	gaa	2057
208	His	Arg	Gln	Asp	Phe	His	Ala	Ile	Val	Pro	Asn	His	Ile	Pro	Glu	Glu	
209			605							610					615		
211	tta	tat	tgg	ggt	gag	gaa	gaa	cat	cag	atc	ttt	aag	aca	ctt	cag	gag	2105
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216	Glu	Arg	Arg	Leu	Arg	Glu	Ala	Ala	Met	Arg	Ala	Lys	Val	Glu	Lys	Thr	
217		635				640						645					
219	gca	ctt	ctg	aaa	act	gaa	aca	aag	gaa	aga	act	atg	aaa	tca	ttt	tta	2201
220	Ala	Leu	Leu	Lys	Thr	Glu	Thr	Lys	Glu	Arg	Thr	Met	Lys	Ser	Phe	Leu	
221	650					655					660				665		
223	ctg	tct	cag	aag	cat	gta	gta	tat	act	gag	cct	ctt	gat	atc	caa	gct	2249
224	Leu	Ser	Gln	Lys	His	Val	Val	Tyr	Thr	Glu	Pro	Leu	Asp	Ile	Gln	Ala	
225				670						675					680		
227	gga	agc	agc	gtc	aca	ggt	tac	tat	aat	ccc	gcc	aat	aca	gta	ctt	aat	2297
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232	Gly	Lys	Pro	Glu	Ile	Trp	Phe	Arg	Cys	Ser	Phe	Asn	Arg	Trp	Thr	His	
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236	Arg	Leu	Gly	Pro	Leu	Pro	Pro	Gln	Lys	Met	Ser	Pro	Ala	Glu	Asn	Gly	
237		715				720						725					
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241	730					735					740				745		
243	gat	ttt	gta	ttt	tcc	gag	aga	gaa	gat	ggt	ggg	att	ttt	gac	aat	aag	2489
244	Asp	Phe	Val	Phe	Ser	Glu	Arg	Glu	Asp	Gly	Gly	Ile	Phe	Asp	Asn	Lys	
245				750						755					760		
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261	810					815					820				825		
263	ttg	aag	atg	aat	aat	gtg	aag	gac	ttt	cgg	ttt	cac	aaa	aac	tac	ttt	2729
264	Leu	Lys	Met	Asn	Asn	Val	Lys	Asp	Phe	Arg	Phe	His	Lys	Asn	Tyr	Phe	
265					830					835					840		
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269				845					850					855			
271	tcg	gtc	tat	ttt	ttg	gag	cct	caa	aac	ggg	tta	ttt	tcg	aaa	ggg	tgc	2825
272	Ser	Val	Tyr	Phe	Leu	Glu	Pro	Gln	Asn	Gly	Leu	Phe	Ser	Lys	Gly	Cys	
273			860					865					870				
275	gtc	tat	ggt	tgt	agc	aat	gat	ggt	gaa	cga	ttt	ggt	ttc	ttc	tgt	cac	2873
276	Val	Tyr	Gly	Cys	Ser	Asn	Asp	Gly	Glu	Arg	Phe	Gly	Phe	Phe	Cys	His	
277		875				880					885						
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280	Ala	Ala	Leu	Glu	Phe	Leu	Leu	Gln	Gly	Gly	Phe	Ser	Pro	Asp	Ile	Ile	
281	890					895				900					905		
283	cat	tgc	cat	gat	tgg	tct	agt	gct	cct	ggt	gct	tgg	ctc	ttt	aag	gaa	2969
284	His	Cys	His	Asp	Trp	Ser	Ser	Ala	Pro	Val	Ala	Trp	Leu	Phe	Lys	Glu	
285				910					915						920		
287	caa	tat	aca	cac	tat	ggt	cta	agc	aaa	tct	cgt	ata	gtc	ttc	acg	ata	3017
288	Gln	Tyr	Thr	His	Tyr	Gly	Leu	Ser	Lys	Ser	Arg	Ile	Val	Phe	Thr	Ile	
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292	His	Asn	Leu	Glu	Phe	Gly	Ala	Asp	Leu	Ile	Gly	Arg	Ala	Met	Thr	Asn	
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297		955					960					965					
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300	Gly	Asn	Pro	Val	Ile	Ala	Pro	His	Leu	His	Lys	Phe	His	Gly	Ile	Val	
301	970					975					980				985		
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309				1005					1010					1015			
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316	Leu	Pro	Leu	Val	Gly	Ile	Ile	Thr	Arg	Leu	Thr	His	Gln	Lys	Gly		
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:48 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:28